

SEQUENCE LISTING

<110> Browse, John et al.

<120> Desaturases and Methods of Using Them for Synthesis of
Polyunsaturated Fatty Acids

<130> 53860

<140>

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<150> 60/111,301

<151> 1998-12-07

<160> 13

<170> PatentIn Ver. 2.0

<210> 1

<211> 1461

<212> DNA

<213> Caenorhabditis elegans

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<210> 2

<211> 447

<212> PRT

<213> Caenorhabditis elegans

<400> 2

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20 25 30
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 35 40 45
 His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu
 50 55 60
 Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys
 65 70 75 80
 Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn
 85 90 95
 Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu
 100 105 110
 Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe
 115 120 125
 Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe
 130 135 140
 Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly
 145 150 155 160
 Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His
 165 170 175
 Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val
 180 185 190
 Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His
 195 200 205
 Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu
 210 215 220
 Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr
 225 230 235 240
 Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His
 245 250 255
 Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser
 260 265 270
 Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg
 275 280 285
 Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp
 290 295 300
 Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met
 305 310 315 320
 Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val
 325 330 335
 Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn
 340 345 350

Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met
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Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln
370 375 380

Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr
385 390 395 400

Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr
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<212> DNA
<213> Euglena gracilis

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aagggatgcc actgatgcct tcatggttat gcactttcaa gaagccttcg acaagctcaa 180
gcgcatgccc aaaatcaatc ccagttttga gttgccaccc caggctgcag tgaatgaagc 240
tcaagaggat ttccggaagc tccgagaaga gttgatcgca actggcatgt ttgatgcctc 300
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cctgatgggt cagtatcaga tgtatttcat tggggcagtg ttgcttgga tgcactatca 420
acagatgggc tggctttctc atgacatttg ccaccaccag actttcaaga accggaactg 480
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ccgcaagctc attcagttcc agcagtacta tttcttggtc atctgtatct tgttgcggtt 720
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<211> 422
<212> PRT
<213> Euglena gracilis

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Ile Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val
 35 40 45
 Met His Phe Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile
 50 55 60
 Asn Pro Ser Phe Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln
 65 70 75 80
 Glu Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe
 85 90 95
 Asp Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly
 100 105 110
 Leu Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe
 115 120 125
 Ile Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu
 130 135 140
 Ser His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn
 145 150 155 160
 Asn Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val
 165 170 175
 Thr Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val
 180 185 190
 Gln Gly His Asp Pro Asp Ile Asp Asn Leu Pro Pro Leu Ala Trp Ser
 195 200 205
 Glu Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln
 210 215 220
 Phe Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile
 225 230 235 240
 Trp Cys Phe Gln Cys Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp
 245 250 255
 Asn Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala
 260 265 270
 Leu His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser
 275 280 285
 Ile Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly
 290 295 300
 Phe Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys
 305 310 315 320
 Ile Gly Asp Pro Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile
 325 330 335
 His Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe
 340 345 350
 Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro

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385						390						395					
Ile	Leu	Leu	Arg	Tyr	Leu	Ala	Val	Phe	Ala	Arg	Met	Ala	Glu	Lys	Gln		
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<210> 5
<211> 27
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: PCR Primer

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<220>  
<221> variation  
<222> (1)..(27)  
<223> y = t or c
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```
<220>
<221> variation
<222> (1)..(27)
<223> n= a, t, c, or g
```

```
<220>
<221> variation
<222> (1)..(27)
<223> r = a or g
```

```
<400> 5
ggctggctga cncaygartt ytgycay
```

27

```
<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: PCR Primer

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<220>  
<221> variation  
<222> (1)..(30)  
<223> n = a, t, g, or c
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<220>  
<221> variation  
<222> (1)..(30)  
<223> r = a or q
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<220>
<221> variation

<222> (1) .. (30)

<223> y = t or c

<400> 6

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30

<210> 7

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primer

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41

<210> 8

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 8

cccgggtgga tccggaacat atcacacgaa acag

34

<210> 9

<211> 6

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Polyadenylation Signal

<400> 9

aauaaa

6

<210> 10

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 10

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20

<210> 11

<211> 9

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Histidine box

<400> 11

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9

<210> 12
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Histidine Box

<220>
<221> VARIANT
<222> (1)..(5)
<223> Xaa = any amino acid

<400> 12
His Xaa Xaa His His
1 5

<210> 13
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Histidine Box

<220>
<221> VARIANT
<222> (1)..(5)
<223> Xaa = any amino acid

<400> 13
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1 5